



Patent Docket No. P1039P1

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- 5 (i) APPLICANT: Chuntharapai, Anon
Kim, Kyung Jin
Love, Richard B.
Lu, Ji

10 (ii) TITLE OF INVENTION: Type I Interferon Receptor Antibodies

(iii) NUMBER OF SEQUENCES: 22

15 (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Genentech, Inc.
(B) STREET: 1 DNA Way
(C) CITY: South San Francisco
(D) STATE: California
(E) COUNTRY: USA
(F) ZIP: 94080

20 (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WinPatin (Genentech)

25 (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE: 07-Apr-1998
(C) CLASSIFICATION:

30 (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/888,140
(B) FILING DATE: 03 July 1997

35 (viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Love, Richard B.
(B) REGISTRATION NUMBER: 34,659
(C) REFERENCE/DOCKET NUMBER: P1039P1

40 (ix) TELECOMMUNICATION INFORMATION:
(A) TELEPHONE: 650/225-5530
(B) TELEFAX: 650/952-9881

45 (2) INFORMATION FOR SEQ ID NO:1:

50 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Arg Trp Asn Arg Ser Asp Glu
1 5 7

5 (2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ala Trp Asn Ala Ser Ala Ala
1 5 7

15 (2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

25 Glu Glu Ile Lys Leu Arg
1 5 6

(2) INFORMATION FOR SEQ ID NO:4:

30 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Ala Ala Ile Ala Leu Ala
1 5 6

40 (2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 5 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

45 Arg Ala Glu Lys Glu
1 5

50 (2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Ala Ala Ala Ala Ala
1 5

10 (2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Glu Val His Leu Glu Ala Glu Asp Lys
20 1 5 9

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Val Ala Leu Ala Ala Ala Ala Ala
30 1 5 9

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Glu Glu Arg Ile Glu
40 1 5

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Ala Ala Ile Ala
1 5

5 (2) INFORMATION FOR SEQ ID NO:11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Arg His Lys Ile Tyr Lys
1 5 6

15 (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

25 Ala Ala Ala Ile Tyr Ala
1 5 6

20 (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

His Leu Tyr Lys Trp Lys
1 5 6

40 (2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

50 Ala Leu Tyr Ala Trp Ala
1 5 6

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Glu Glu Ile Lys Phe Asp Thr Glu
1 5 8

10 (2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

Ala Ala Ile Ala Phe Ala Thr Ala
20 1 5 8

(2) INFORMATION FOR SEQ ID NO:17:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Glu Arg Lys Ile Ile Glu Lys Lys
1 5 8

30 (2) INFORMATION FOR SEQ ID NO:18:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Ala Ala Ala Ile Ile Ala Ala Ala
1 5 8

40 (2) INFORMATION FOR SEQ ID NO:19:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6 amino acids
 - (B) TYPE: Amino Acid
 - (D) TOPOLOGY: Linear

45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Asp Glu Lys Leu Asn Lys
1 5 6

5 (2) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: Amino Acid
(D) TOPOLOGY: Linear

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Ala Ala Ala Leu Asn Ala
1 5 6

15 (2) INFORMATION FOR SEQ ID NO:21:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6741 base pairs
(B) TYPE: Nucleic Acid
(C) STRANDEDNESS: Double
(D) TOPOLOGY: Linear

20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

25 GAATTCCGTA ACTGGTGGGA TCTGCGCGG CTCCCAGATG ATGGTCGTCC 50

30 TCCTGGCGC GACGACCCTA GTGCTCGTCG CCGTGGCGCC ATGGGTGTTG 100

TCCGCAGCCG CAGGTGGAAA AAATCTAAAA TCTCCTCAAA AAGTAGAGGT 150

CGACATCATA GATGACAAC TTATCCTGAG GTGGAACAGG AGCGATGAGT 200

35 CTGTCGGGAA TGTGACTTT TCATTCGATT ATCAAAAAAC TGGGATGGAT 250

AATTGGATAA AATTGTCTGG GTGTCAGAAT ATTACTAGTA CCAAATGCAA 300

40 CTTTTCTTCA CTCAAGCTGA ATGTTATGA AGAAATTAAA TTGCGTATAA 350

GAGCAGAAAA AGAAAACACT TCTTCATGGT ATGAGGTTGA CTCATTTACA 400

CCATTTCGCA AAGCTCAGAT TGGTCCTCCA GAAGTACATT TAGAAGCTGA 450

45 AGATAAGGCA ATAGTGATAC ACATCTCTCC TGGAACAAAA GATAGTGTAA 500

TGTGGGCTTT GGATGGTTA AGCTTTACAT ATAGCTTACT TATCTGGAAA 550

AACTCTTCAG GTGTAGAAGA AAGGATTGAA AATATTTATT CCAGACATAA 600

50 AATTTATAAA CTCTCACCAAG AGACTACTTA TTGTCTAAAA GTTAAAGCAG 650

CACTACTTAC GTCATGGAAA ATTGGTGTCT ATAGTCCAGT ACATTGTATA 700

AAGACCACAG TTGAAAATGA ACTACCTCCA CCAGAAAATA TAGAAGTCAG 750
TGTCCAAAAT CAGAACTATG TTCTTAAATG GGATTATACA TATGCAAACA 800
5 TGACCTTCA AGTCAGTGG CTCCACGCCT TTTAAAAAG GAATCCTGGA 850
AACCATTGT ATAAATGGAA ACAAAATACCT GACTGTGAAA ATGTCAAAAC 900
10 TACCCAGTGT GTCTTCCTC AAAACGTTT CCAAAAAGGA ATTTACCTTC 950
TCCCGCTACA AGCATCTGAT GGAAATAACA CATCTTTTG GTCTGAAGAG 1000
ATAAAGTTG ATACTGAAAT ACAAGCTTTC CTACTTCCTC CAGTCTTAA 1050
15 CATTAGATCC CTTAGTGATT CATTCCATAT CTATATCGGT GCTCCAAAAC 1100
AGTCTGGAAA CACGCCGTG ATCCAGGATT ATCCACTGAT TTATGAAATT 1150
20 ATTTTTGGG AAAACACTTC AAATGCTGAG AGAAAAATTA TCGAGAAAAA 1200
AACTGATGTT ACAGTTCTA ATTTGAAACC ACTGACTGTA TATTGTGTGA 1250
AAGCCAGAGC ACACACCATG GATGAAAAGC TGAATAAAAG CAGTGTTTT 1300
25 AGTGACGCTG TATGTGAGAA AACAAAACCA GGAAATGACA AAACTCACAC 1350
ATGCCAACCG TGCCCAGCAC CTGAACTCCT GGGGGACCG TCAGTCTTCC 1400
30 TCTTCCCCCC AAAACCAAG GACACCCTCA TGATCTCCCG GACCCCTGAG 1450
GTCACATGCG TGGTGGTGGA CGTGAGCCAC GAAGACCCTG AGGTCAAGTT 1500
CAACTGGTAC GTGGACGGCG TGGAGGTGCA TAATGCCAAG ACAAAAGCCGC 1550
35 GGGAGGAGCA GTACAACAGC ACGTACCGAG TGGTCAGCGT CCTCACCGTC 1600
CTGCACCAGG ACTGGCTGAA TGGCAAGGAG TACAAGTGCA AGGTCTCCAA 1650
40 CAAAGCCCTC CCAGCCCCCA TCGAGAAAAC CATCTCCAAA GCCAAAGGGC 1700
AGCCCCGAGA ACCACAGGTG TACACCCTGC CCCCATCCCG GGAAGAGATG 1750
ACCAAGAACCC AGGTCAGCCT GACCTGCCTG GTCAAAGGCT TCTATCCAG 1800
45 CGACATCGCC GTGGAGTGGG AGAGCAATGG GCAGCCGGAG AACAACTACA 1850
AGACCACGCC TCCCGTGCTG GACTCCGACG GCTCCTTCTT CCTCTACAGC 1900
50 AAGCTCACCG TGGACAAGAG CAGGTGGCAG CAGGGGAACG TCTTCTCATG 1950
CTCCGTGATG CATGAGGCTC TGCACAAACCA CTACACCGCAG AAGAGCCTCT 2000
CCCTGTCTCC GGGTAAATGA GTGCGACGGC CCTAGAGTCG ACCTGCAGAA 2050

GCTTAGAAC C GAGGGGCCGC CATGGCCCAA CTTGTTTATT GCAGCTTATA 2100
ATGGTTACAA ATAAAGCAAT AGCATCACAA ATTCACAAA TAAAGCATT 2150
5 TTTTCACTGC ATTCTAGTTG TGGTTGTCC AACTCATCA ATGTATCTTA 2200
TCATGTCTGG ATCGATCGGG AATTAATTG GCGCAGCACC ATGGCCTGAA 2250
ATAACCTCTG AAAGAGGAAC TTGGTTAGGT ACCTTCTGAG GCGGAAAGAA 2300
10 CCAGCTGTGG AATGTGTGTC AGTTAGGGTG TGGAAAGTCC CCAGGCTCCC 2350
CAGCAGGCAG AAGTATGCAA AGCATGCATC TCAATTAGTC AGCAACCAGG 2400
15 TGTGGAAAGT CCCCAGGCTC CCCAGCAGGC AGAAGTATGC AAAGCATGCA 2450
TCTCAATTAG TCAGCAACCA TAGTCCCGCC CCTAACTCCG CCCATCCCGC 2500
20 CCCTAACTCC GCCCAGTTCC GCCCATTCTC CGCCCCATGG CTGACTAATT 2550
TTTTTTATTT ATGCAGAGGC CGAGGCCGCC TCGGCCTCTG AGCTATTCCA 2600
GAAGTAGTGA GGAGGCTTT TTGGAGGCCT AGGTTTTGC AAAAGCTGT 2650
25 TAACAGCTTG GCACTGGCCG TCGTTTACA ACGTCGTGAC TGGGAAAACC 2700
CTGGCGTTAC CCAACTTAAT CGCCTTGCAG CACATCCCC CTTGCCAGC 2750
30 TGGCGTAATA GCGAAGAGGC CCGCACCGAT CGCCCTTCCC AACAGTTGCG 2800
TAGCCTGAAT GGCGAATGGC GCCTGATGCG GTATTTCTC CTTACGCATC 2850
TGTGCGGTAT TTCACACCGC ATACGTAAA GCAACCATAG TACGCGCCCT 2900
35 GTAGCGGCGC ATTAAGCGCG GCGGGTGTGG TGGTTACGCG CAGCGTGACC 2950
GCTACACTTG CCAGCGCCCT AGCGCCCGCT CCTTCGCTT TCTTCCCTTC 3000
40 CTTTCTCGCC ACGTTCGCCG GCTTCCCCG TCAAGCTCTA AATCGGGGGC 3050
TCCCTTAGG GTTCCGATTT AGTGCTTAC GGCACCTCGA CCCCCAAAAAA 3100
CTTGATTGG GTGATGGTTC ACGTAGTGGG CCATGCCCT GATAGACGGT 3150
45 TTTTCGCCCT TTGACGTTGG AGTCCACGTT CTTAATAGT GGACTCTTGT 3200
TCCAAACTGG AACAAACACTC AACCTATCT CGGGCTATTTC TTTGATTAA 3250
50 TAAGGGATTT TGCCGATTTG GGCCTATTGG TTAAAAAAATG AGCTGATTAA 3300
ACAAAAAATTT AACGCGAATT TTAACAAAAT ATTAACGTTT ACAATTAT 3350
GGTGCACTCT CAGTACAATC TGCTCTGATG CCGCATAGTT AAGCCAACTC 3400

CGCTATCGCT ACGTGAUTGG GTCATGGCTG CGCCCCGACA CCCGCCAACA 3450
CCCGCTGACG CGCCCTGACG GGCTTGCTG CTCCCGGCAT CCGCTTACAG 3500
5 ACAAGCTGTG ACCGTCTCCG GGAGCTGCAT GTGTCAGAGG TTTTCACCGT 3550
CATCACCGAA ACAGCGAGG CAGTATTCTT GAAGACGAAA GGGCCTCGTG 3600
10 ATACGCCTAT TTTTATAGGT TAATGTCATG ATAATAATGG TTTCTTAGAC 3650
GTCAGGTGGC ACTTTCGGG GAAATGTGCG CGGAACCCCT ATTTGTTTAT 3700
TTTTCTAAAT ACATTCAAAT ATGTATCCGC TCATGAGACA ATAACCCTGA 3750
15 TAAATGCTTC AATAATATTG AAAAAGGAAG AGTATGAGTA TTCAACATTT 3800
CCGTGTCGCC CTTATTCCCT TTTTGCGGC ATTTGCCTT CCTGTTTTG 3850
20 CTCACCCAGA AACGCTGGTG AAAGTAAAAG ATGCTGAAGA TCAGTTGGGT 3900
GCACGAGTGG GTTACATCGA ACTGGATCTC AACAGCGGTAAAGATCCTTGA 3950
GAGTTTCGC CCCGAAGAAC GTTTCCAAT GATGAGCACT TTTAAAGTTC 4000
25 TGCTATGTGG CGCGGTATTA TCCC GTGATG ACGCCGGCA AGAGCAACTC 4050
GGTCGCCGCA TACACTATTTC TCAGAATGAC TTGGTTGAGT ACTCACCAGT 4100
CACAGAAAAG CATCTTACGG ATGGCATGAC AGTAAGAGAA TTATGCAGTG 4150
30 CTGCCATAAC CATGAGTGAT AACACTGCGG CCAACTTAAC TCTGACAACG 4200
ATCGGAGGAC CGAAGGAGCT AACCGCTTTT TTGCACAACA TGGGGGATCA 4250
35 TGTAACTCGC CTTGATCGTT GGGAAACCGGA GCTGAATGAA GCCATACCAA 4300
ACGACGAGCG TGACACCACG ATGCCAGCAG CAATGGCAAC AACGTTGCGC 4350
40 AAACTATTAA CTGGCGAACT ACTTACTCTA GCTTCCCGGC AACAAATTAAAT 4400
AGACTGGATG GAGGCGGATA AAGTTGCAGG ACCACTTCTG CGCTCGGCC 4450
TTCCGGCTGG CTGGTTTATT GCTGATAAT CTGGAGCCGG TGAGCGTGGG 4500
45 TCTCGCGGTA TCATTGCAGC ACTGGGGCCA GATGGTAAGC CCTCCCGTAT 4550
CGTAGTTATC TACACGACGG GGAGTCAGGC AACTATGGAT GAAACGAAATA 4600
50 GACAGATCGC TGAGATAGGT GCCTCACTGA TTAAGCATTG GTAACTGTCA 4650
GACCAAGTTT ACTCATATAT ACTTTAGATT GATTAAAAAC TTCATTTTA 4700
ATTTAAAAGG ATCTAGGTGA AGATCCTTT TGATAATCTC ATGACCAAAA 4750

TCCCTTAACG TGAGTTTCG TTCCACTGAG CGTCAGACCC CGTAGAAAAG 4800
ATCAAAGGAT CTTCTTGAGA TCCTTTTTT CTGCGCGTAA TCTGCTGCTT 4850
5 GCAAACAAAA AAACCACCGC TACCAGCGGT GGTTTGTGG CC GGATCAAG 4900
AGCTACCAAC TCTTTTCCG AAGGTAACTG GCTTCAGCAG AGCGCAGATA 4950
10 CCAAATACTG TCCTTCTAGT GTAGCCGTAG TTAGGCCACC ACTTCAAGAA 5000
CTCTGTAGCA CCGCCTACAT ACCTCGCTCT GCTAATCCTG TTACCAGTGG 5050
CTGCTGCCAG TGGCGATAAG TCGTGTCTTA CCGGGTTGGA CTCAAGACGA 5100
15 TAGTTACCGG ATAAGGCGCA GCGGTCGGGC TGAACGGGGG GTTCGTGCAC 5150
ACAGCCCAGC TTGGAGCGAA CGACCTACAC CGAACTGAGA TACCTACAGC 5200
20 GTGAGCATTG AGAAAGCGCC ACGCTTCCCG AAGGGAGAAA GGCGGACAGG 5250
TATCCGGTAA GCGGCAGGGT CGGAACAGGA GAGCGCACGA GGGAGCTTCC 5300
AGGGGGAAAC GCCTGGTATC TTTATAGTCC TGTCGGTTT CGCCACCTCT 5350
25 GACTTGAGCG TCGATTTTG TGATGCTCGT CAGGGGGCG GAGCCTATGG 5400
AAAAACGCCA GCAACGCGGC CTTTTACGG TTCCTGGCCT TTTGCTGGCC 5450
30 TTTGCTCAC ATGTTCTTC CTGCGTTATC CCCTGATTCT GTGGATAACC 5500
GTATTACCGC CTTTGAGTGA GCTGATAACCG CTCGCCGCAG CCGAACGACC 5550
GAGCGCAGCG AGTCAGTGAG CGAGGAAGCG GAAGAGCGCC CAATACGCAA 5600
35 ACCGCCTCTC CCCGCGCGTT GGCGATTCA TTAATCCAGC TGGCACGACA 5650
GGTTTCCCGA CTGGAAAGCG GGCAGTGAGC GCAACGCAAT TAATGTGAGT 5700
40 TACCTCACTC ATTAGGCACC CCAGGCTTTA CACTTATGC TTCCGGCTCG 5750
TATGTTGTGT GGAATTGTGA GCGGATAACA ATTCACACA GGAAACAGCT 5800
ATGACCATGA TTACGAATTA ATTGAGCTC GCCCGACATT GATTATTGAC 5850
45 TAGTTATTAA TAGTAATCAA TTACGGGTC ATTAGTCAT AGCCCATATA 5900
TGGAGTTCCG CGTTACATAA CTTACGGTAA ATGGCCCGCC TGGCTGACCG 5950
50 CCCAACGACC CCCGCCATT GACGTCAATA ATGACGTATG TTCCCATAGT 6000
AACGCCATAA GGGACTTTCC ATTGACGTCA ATGGGTGGAG TATTTACGGT 6050
AAACTGCCCA CTTGGCAGTA CATCAAGTGT ATCATATGCC AAGTACGCC 6100

CCTATTGACG TCAATGACGG TAAATGGCCC GCCTGGCATT ATGCCAGTA 6150
 CATGACCTTA TGGGACTTTC CTACTTGCA GTACATCTAC GTATTAGTCA 6200
 5 TCGCTATTAC CATGGTGATG CGGTTTGGC AGTACATCAA TGGCGTGGA 6250
 TAGCGGTTG ACTCACGGGG ATTTCCAAGT CTCCACCCCA TTGACGTCAA 6300
 10 TGGGAGTTG TTTGGCACC AAAATCAACG GGACTTTCCA AAATGTCGTA 6350
 ACAACTCCGC CCCATTGACG CAAATGGCG GTAGGCGTGT ACGGTGGAG 6400
 GTCTATATAA GCAGAGCTCG TTTAGTGAAC CGTCAGATCG CCTGGAGACG 6450
 15 CCATCCACGC TGTTTGACC TCCATAGAAC ACACCGGGAC CGATCCAGCC 6500
 TCCGCGGCCG GGAACGGTGC ATTGGAACGC GGATTCCCCG TGCCAAGAGT 6550
 20 GACGTAAGTA CCGCCTATAG AGTCTATAGG CCCACCCCT TGGCTCGTTA 6600
 GAACGCGGCT ACAATTAATA CATAACCTTA TGTATCATAC ACATACGATT 6650
 TAGGTGACAC TATAGAATAA CATCCACTTT GCCTTTCTCT CCACAGGTGT 6700
 25 CCACTCCCAG GTCCAAGTGC AGGCCATGGC GGCCATCGAT T 6741

(2) INFORMATION FOR SEQ ID NO:22:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 631 amino acids
- (B) TYPE: Amino Acid
- (D) TOPOLOGY: Linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

35	Leu	Lys	Ser	Pro	Gln	Lys	Val	Glu	Val	Asp	Ile	Ile	Asp	Asp	Asn
	1				5				10				15		
	Phe	Ile	Leu	Arg	Trp	Asn	Arg	Ser	Asp	Glu	Ser	Val	Gly	Asn	Val
40					20			25					30		
	Thr	Phe	Ser	Phe	Asp	Tyr	Gln	Lys	Thr	Gly	Met	Asp	Asn	Trp	Ile
45					35			40			45				
	Lys	Leu	Ser	Gly	Cys	Gln	Asn	Ile	Thr	Ser	Thr	Lys	Cys	Asn	Phe
					50			55				60			
	Ser	Ser	Leu	Lys	Leu	Asn	Val	Tyr	Glu	Glu	Ile	Lys	Leu	Arg	Ile
					65			70			75				
50	Arg	Ala	Glu	Lys	Glu	Asn	Thr	Ser	Ser	Trp	Tyr	Glu	Val	Asp	Ser
					80			85			90				
	Phe	Thr	Pro	Phe	Arg	Lys	Ala	Gln	Ile	Gly	Pro	Pro	Glu	Val	His
					95			100			105				

	Leu Glu Ala Glu Asp Lys Ala Ile Val Ile His Ile Ser Pro Gly		
	110	115	120
5	Thr Lys Asp Ser Val Met Trp Ala Leu Asp Gly Leu Ser Phe Thr		
	125	130	135
	Tyr Ser Leu Leu Ile Trp Lys Asn Ser Ser Gly Val Glu Glu Arg		
	140	145	150
10	Ile Glu Asn Ile Tyr Ser Arg His Lys Ile Tyr Lys Leu Ser Pro		
	155	160	165
15	Glu Thr Thr Tyr Cys Leu Lys Val Lys Ala Ala Leu Leu Thr Ser		
	170	175	180
	Trp Lys Ile Gly Val Tyr Ser Pro Val His Cys Ile Lys Thr Thr		
	185	190	195
20	Val Glu Asn Glu Leu Pro Pro Pro Glu Asn Ile Glu Val Ser Val		
	200	205	210
	Gln Asn Gln Asn Tyr Val Leu Lys Trp Asp Tyr Thr Tyr Ala Asn		
	215	220	225
25	Met Thr Phe Gln Val Gln Trp Leu His Ala Phe Leu Lys Arg Asn		
	230	235	240
30	Pro Gly Asn His Leu Tyr Lys Trp Lys Gln Ile Pro Asp Cys Glu		
	245	250	255
	Asn Val Lys Thr Thr Gln Cys Val Phe Pro Gln Asn Val Phe Gln		
	260	265	270
35	Lys Gly Ile Tyr Leu Leu Arg Val Gln Ala Ser Asp Gly Asn Asn		
	275	280	285
	Thr Ser Phe Trp Ser Glu Glu Ile Lys Phe Asp Thr Glu Ile Gln		
	290	295	300
40	Ala Phe Leu Leu Pro Pro Val Phe Asn Ile Arg Ser Leu Ser Asp		
	305	310	315
45	Ser Phe His Ile Tyr Ile Gly Ala Pro Lys Gln Ser Gly Asn Thr		
	320	325	330
	Pro Val Ile Gln Asp Tyr Pro Leu Ile Tyr Glu Ile Ile Phe Trp		
	335	340	345
50	Glu Asn Thr Ser Asn Ala Glu Arg Lys Ile Ile Glu Lys Lys Thr		
	350	355	360
	Asp Val Thr Val Pro Asn Leu Lys Pro Leu Thr Val Tyr Cys Val		
	365	370	375

	Lys Ala Arg Ala His Thr Met Asp Glu Lys Leu Asn Lys Ser Ser		
	380	385	390
5	Val Phe Ser Asp Ala Val Cys Glu Lys Thr Lys Pro Gly Asn Asp		
	395	400	405
	Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly		
10	410	415	420
	Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu		
	425	430	435
15	Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val		
	440	445	450
	Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly		
	455	460	465
20	Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr		
	470	475	480
	Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln		
25	485	490	495
	Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys		
	500	505	510
30	Ala Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly		
	515	520	525
	Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu		
	530	535	540
35	Glu Met Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly		
	545	550	555
	Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln		
40	560	565	570
	Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp		
	575	580	585
45	Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg		
	590	595	600
	Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala		
	605	610	615
50	Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser Pro Gly		
	620	625	630
	Lys		
	631		